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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=10; day=21; hr=10; min=55; sec=1; ms=429; ]

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Application No: 10559986 Version No: 3.0

**Input Set:**

**Output Set:**

**Started:** 2009-10-05 16:44:05.420  
**Finished:** 2009-10-05 16:44:10.734  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 314 ms  
**Total Warnings:** 46  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 100  
**Actual SeqID Count:** 100

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
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W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
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W 213	Artificial or Unknown found in <213> in SEQ ID (29)
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**Input Set:**

**Output Set:**

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Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (57)
W 402	Undefined organism found in <213> in SEQ ID (58)
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W 402	Undefined organism found in <213> in SEQ ID (83)
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SEQUENCE LISTING

<110> Nestec S.A.; Cornell Research Foundation, Inc.

<120> Modulation Of Coffee Flavour Precursor Levels In Green Coffee Grains

<130> PAT 60100W-1

<140> 10559986

<141> 2006-09-11

<150> EP 03394056.0

<151> 2003-06-20

<160> 100

<170> PatentIn version 3.5

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<213> Coffea canephora

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<221> mRNA

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Met Met Met Thr Ser Gly Gly Leu Met Leu Thr Cys Thr Leu Ala Ile

1 5 10 15

acc ctc tta tcc tgc gca ctc atc tct tca acc act ttc caa cat gaa 217

Thr Leu Leu Ser Cys Ala Leu Ile Ser Ser Thr Thr Phe Gln His Glu

20 25 30

att cag tat cga gta caa gac ccg tta atg ata cgc caa gtc acc gac 265

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35 40 45

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tac gag aaa act tac tct acg cac gag gag tac gtg cac cgc ctg ggg	409
Tyr Glu Lys Thr Tyr Ser Thr His Glu Glu Tyr Val His Arg Leu Gly	
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ccc tcc gca atc cac ggc gtc acc cag ttc tct gat ctc acc gag gag	505
Pro Ser Ala Ile His Gly Val Thr Gln Phe Ser Asp Leu Thr Glu Glu	
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Gly Thr Thr Gln Leu Gly Lys Asp Asp Gly Asp Glu Ser Ala Ala Glu	
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Val Met Met Asp Val Ser Asp Leu Pro Glu Ser Phe Asp Trp Arg Glu	
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195 200 205	
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Thr Gly Lys Leu Leu Ser Leu Ser Glu Gln Gln Leu Val Asp Cys Asp	
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225 230 235 240	
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Gly Gly Leu Met Thr Thr Ala Phe Asn Tyr Leu Ile Glu Ala Gly Gly	
245 250 255	
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Ile Glu Glu Glu Val Thr Tyr Pro Tyr Thr Gly Lys Arg Gly Glu Cys	
260 265 270	
aaa ttc aat cct gag aaa gtt gcg gtg aaa gtg cgg aat ttc gca aaa	985
Lys Phe Asn Pro Glu Lys Val Ala Val Lys Val Arg Asn Phe Ala Lys	
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ccg ctt gct att gga ttg aat gcg gta ttc atg caa act tac atc ggg			1081
Pro Leu Ala Ile Gly Leu Asn Ala Val Phe Met Gln Thr Tyr Ile Gly			
305	310	315	320
ggt gtg tca tgt cct att tgt gac aaa aag agg atc aac cat ggt			1129
Gly Val Ser Cys Pro Leu Ile Cys Asp Lys Lys Arg Ile Asn His Gly			
325	330	335	
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Val Leu Leu Val Gly Tyr Gly Ser Arg Gly Phe Ser Ile Leu Arg Leu			
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Gly Tyr Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Lys Arg Trp			
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Gly Glu His Gly Cys Tyr Arg Leu Cys Arg Gly His Asn Met Cys Gly			
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Asn His His His Arg His His Pro Gly Arg Ser Ser Ala Asn His Arg			
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Ile Phe Ala Lys Asn Leu Ile Lys Ala Ala Glu His Gln Ala Met Asp  
100 105 110

Pro Ser Ala Ile His Gly Val Thr Gln Phe Ser Asp Leu Thr Glu Glu  
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Gly Thr Thr Gln Leu Gly Lys Asp Asp Gly Asp Glu Ser Ala Ala Glu  
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Val Met Met Asp Val Ser Asp Leu Pro Glu Ser Phe Asp Trp Arg Glu  
165 170 175

Lys Gly Ala Val Thr Glu Val Lys Thr Gln Gly Arg Cys Gly Ser Cys  
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Trp Ala Phe Ser Thr Thr Gly Ala Ile Glu Gly Ala Asn Phe Ile Ala  
195 200 205

Thr Gly Lys Leu Leu Ser Leu Ser Glu Gln Gln Leu Val Asp Cys Asp  
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His Met Cys Asp Leu Lys Glu Lys Asp Asp Cys Asp Asp Gly Cys Ser  
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Gly Gly Leu Met Thr Thr Ala Phe Asn Tyr Leu Ile Glu Ala Gly Gly  
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Ile Glu Glu Glu Val Thr Tyr Pro Tyr Thr Gly Lys Arg Gly Glu Cys  
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Lys Phe Asn Pro Glu Lys Val Ala Val Lys Val Arg Asn Phe Ala Lys  
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Ile Pro Glu Asp Glu Ser Gln Ile Ala Ala Asn Val Val His Asn Gly  
290 295 300

Pro Leu Ala Ile Gly Leu Asn Ala Val Phe Met Gln Thr Tyr Ile Gly  
305 310 315 320

Gly Val Ser Cys Pro Leu Ile Cys Asp Lys Lys Arg Ile Asn His Gly  
325 330 335

Val Leu Leu Val Gly Tyr Gly Ser Arg Gly Phe Ser Ile Leu Arg Leu  
340 345 350

Gly Tyr Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Lys Arg Trp  
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Met Ala Lys Pro Ser Ser Ser Leu Leu Thr Leu  
1 5 10

cct tcc ttt ctt ctg atc ttt ttc att ctt gca cta ttt tcc acc acc 159  
Pro Ser Phe Leu Leu Ile Phe Phe Ile Leu Ala Leu Phe Ser Thr Thr  
15 20 25

ctc caa gtt aat gcc ttg gga agg aaa gtg gga gca agg gag aag att 207  
Leu Gln Val Asn Ala Leu Gly Arg Lys Val Gly Ala Arg Glu Lys Ile  
30 35 40

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Glu Asp Val Lys Ser Asn Lys Glu Val Gln Glu Leu Gly Glu Tyr Cys		
45	50	55
gtt tct gag tac aac aag agt ttg cgg aag aac aac gaa agt ggt		303
Val Ser Glu Tyr Asn Lys Ser Leu Arg Lys Asn Asn Glu Ser Gly		
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75		
gct cct ata atc ttc aca tct gtg gtg gag gct gag aag cag gtg gtt		351
Ala Pro Ile Ile Phe Thr Ser Val Val Glu Ala Glu Lys Gln Val Val		
80	85	90
gct ggg atc aaa tat tat ctc aag att aag gcc acc act tct tct ggg		399
Ala Gly Ile Lys Tyr Tyr Leu Lys Ile Lys Ala Thr Thr Ser Ser Gly		
95	100	105
gtt ccc aag gtt tac gat gcc att gtg gtg gtt cgg cct tgg gtt cat		447
Val Pro Lys Val Tyr Asp Ala Ile Val Val Val Arg Pro Trp Val His		
110	115	120
act aag cca agg cag ttg ctc aac ttc tcc cct tcc cct gcc act aaa		495
Thr Lys Pro Arg Gln Leu Leu Asn Phe Ser Pro Ser Pro Ala Thr Lys		
125	130	135
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attatttagta ccttcagtg caaattctct ttgctgttaa gtgttcggtt tttttttttt		608
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20	25	30

Leu Gly Arg Lys Val Gly Ala Arg Glu Lys Ile Glu Asp Val Lys Ser		
35	40	45

Asn Lys Glu Val Gln Glu Leu Gly Glu Tyr Cys Val Ser Glu Tyr Asn		
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Lys Ser Leu Arg Lys Lys Asn Asn Glu Ser Gly Ala Pro Ile Ile Phe  
65 70 75 80

Thr Ser Val Val Glu Ala Glu Lys Gln Val Val Ala Gly Ile Lys Tyr  
85 90 95

Tyr Leu Lys Ile Lys Ala Thr Thr Ser Ser Gly Val Pro Lys Val Tyr  
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Asp Ala Ile Val Val Val Arg Pro Trp Val His Thr Lys Pro Arg Gln  
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aaaaatccat tcttggaaatt catttatcca tatacaccat acttgtgcat gtccctttg 180  
gttgtttgc ttttgtata agtaattgtt ggttattgg ttttcatga tggctccgga 240  
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tgttattttt gatgtagaag gtaacaataa tgtgggtttt gaggtggaaac ataaattaa 360  
agggagaagg aatgagaatg gaggaagagg gtcttttga cttcaactaa ggctcatgat 420  
tcccacccgcc atggcaga atg ctt gca gcc ctt gac atg cct ttg ggt ggc 471  
Met Leu Ala Ala Leu Asp Met Pro Leu Gly Gly  
1 5 10

aat ggt tcc cct aca gat gca gcg ctc tat ttc act aag ctt tcg att 519  
Asn Gly Ser Pro Thr Asp Ala Ala Leu Tyr Phe Thr Lys Leu Ser Ile

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Gly Thr Pro Pro Gln Asp Tyr Tyr Val Gln Val Asp Thr Gly Ser Asp			
30	35	40	
att ctc tgg gta aac tgt gct ggt tgt gtc aga tgc ccc aag aaa agc			615
Ile Leu Trp Val Asn Cys Ala Gly Cys Val Arg Cys Pro Lys Lys Ser			
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agt ctt ggt att gac ttg act cta tat gac atg aaa gcc tcc agc acc			663
Ser Leu Gly Ile Asp Leu Thr Leu Tyr Asp Met Lys Ala Ser Ser Thr			
60	65	70	75
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Gly Arg Leu Val Thr Cys Asp Gln Asp Phe Cys Leu Ser Ala Phe Asn			
80	85	90	
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Ala Pro Ala Ser Asp Cys Lys Val Gly Asn Pro Cys Ala Tyr Ser Val			
95	100	105	
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Thr Tyr Gly Asp Gly Ser Ser Thr Gly Gly Tyr Phe Val Arg Asp Tyr			
110	115	120	
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Ala Lys Leu Asn Gln Leu Thr Gly Asn Leu Gln Thr Ile Pro Met Asn			
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Gly Ser Ile Val Phe Gly Cys Ser Ser Gln Gln Ser Gly Glu Leu Gly			
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Ser Ser Thr Glu Ala Val Asp Gly Ile Ile Gly Phe Gly Gln Ala Asn			
160	165	170	
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Phe Ser His Cys Leu Asp Gly Ile Asn Gly Gly Ile Phe Ala Ile			
190	195		